

REMARKS

The above amendments to the above-captioned application along with the following remarks are being submitted as a full and complete response to the Official Action dated December 23, 2005. In view of the above amendments and the following remarks, the Examiner is respectfully requested to give due consideration to this application, to indicate the allowability of the claims, and to pass this case to issue.

Status of the Claims

Claims 1-15 are under consideration in this application. Claims 5-6, 8, 12 and 14-15 are being amended, as set forth in the above marked-up presentation of the claim amendments, in order to more particularly define and distinctly claim applicants' invention.

The claims are being amended to correct formal errors and/or to better recite or describe the features of the present invention as claimed. All the amendments to the claims are supported by the specification. Applicants hereby submit that no new matter is being introduced into the application through the submission of this response.

Formality Rejections

Claims 5-7, 12, 14 and 15 were rejected under 35 U.S.C. §112, first paragraph, for reciting “searching within ~~biopolymer~~ attribute information of biopolymers contained in the selected subtree for biopolymers whose attribute information contains the designated keyword”, which the Examiner considers to be new matter, and further under 35 U.S.C. §112, second paragraph, for being indefinite.

Regarding the new matter rejection, Applicants respectfully contend that the recitation is not new matter, but is fully supported by (1) the recitation of the Step 2305 “*Search for gene information: Is keyword of search[i].keyword present in the attribute of gene_info corresponding to targetClust.geneID?*” in the diamond of Fig. 23, (2) the description of “*When it is leaf, the following process is repeated until gene information corresponding to leaf is completely compared with the keyword read out from the keyword dictionary file. In other word, the process is repeated until i becomes key_num (Step 2304). First the attribute of gene information structure gene_infor corresponding to targetClust.geneID is evaluated as to inclusion of keyword search[i].keyword (Step 2305).*” on page 27, last paragraph of the specification, (3) “Gene information” in Fig. 1, and (4) the description of “*information of each of the observed genes is listed on the right hand side*” on page 2, last paragraph.

Regarding the indefiniteness rejection, as the claims are being amended as required by the Examiner, the withdrawal of the outstanding informality rejections is in order, and is therefore respectfully solicited.

Prior Art Discussion

The Examiner rejected claims 1-3 under 35 U.S.C. 102(b) as being anticipated by an article by Michaels (Pacific Symposium on Biocomputing (1998) vol. 3, pp. 42-53; hereinafter "Michaels"). This rejection has been carefully considered, but is most respectfully traversed as follows.

The method for displaying a dendrogram comprises the steps of: clustering a plurality of biopolymers with a first clustering method which is based on a set of gene expression data obtained by experiments on the plurality of biopolymers, and displaying clustering results thereof in a form of a dendrogram in a display window; selecting a subtree in the dendrogram in the display window; Claim 1: displaying the selected subtree in a separate display window (Fig. 6; p. 7, last paragraph) or Claim 3: replacing the selected subtree with an icon 701 in the dendrogram (Fig. 7; p. 8, 2nd paragraph) thereby displaying the dendrogram with the icon rather than with the selected subtree (*"The subtree 505 can be replaced with an icon 701, by which a global state of the dendrogram can readily be observed"* p. 8, lines 16-17; Fig. 7); grouping biopolymers in the selected subtree in the separate display window into at least one function group sharing one of functional characteristics consisting of enzymatic (p.2, line 5), metabolic (p. 2, line 6), transporting (Fig. 11), and cell cycle (Fig. 13) functions (*"gene groups with similar functions"* p. 8, lines 17-18; *"genes belonging to the same cluster may possibly share common functional characteristics"* p. 3, line 7-8; *"function units or function groups are also analyzed by correlating with known enzymatic reaction data or metabolism data"* p. 2, lines 4-6; Function 1104: CELL CYCLE in Fig. 11; Function: TRANSPORT in Fig. 13); and displaying said function group of biopolymers in the separate display window. Claim 2 recites an additional step of designating a second clustering method, which is different from the first clustering method, for further clustering the biopolymers in the selected subtree in the separate display window (*"selecting a subtree and then subjecting the selected subtree to another clustering method"* p. 4, lines 22-23).

The method for displaying a dendrogram of claims 5-6 comprises the same clustering, subtree-selecting, grouping, and function group displaying steps of claims 1 and 3, along with the following additional steps.

Claim 5 further recites searching in the selected subtree for keywords available in a keyword dictionary file (“Figure 8 is a view showing an exemplary screen displayed upon selecting a command ‘search for keyword contained in this subtree’ from the menu shown in Figure 5. Among genes contained in the selected subtree, genes having gene information with predetermined keywords are counted and the results are displayed as search results 801” p. 8, last paragraph; Fig. 16; “Fig. 16 is a diagram showing an example of a search structure for storing a query of search and its results. For each keyword registered in the keyword dictionary file 906, a single structure is generated” p. 18, lines 18-21); counting biopolymers in the selected subtree whose attribute information contains at least one of the searched keywords and displaying each of the searched keywords with a corresponding count of the biopolymers whose attribute information contains at least one of the searched keywords (p. 8, lines 23-25); grouping biopolymers in the selected subtree into at least one function group sharing one of functional characteristics consisting of enzymatic, metabolic, transporting, and cell cycle functions; displaying said function group of biopolymers in the display window; displaying the searched keywords and said count in a separated display window on top of the display window displaying said function group of biopolymers therein (Fig. 8); highlighting in the display window a location of each of the biopolymers in the selected subtree whose attribute information contains the searched keywords (e.g., “When a keywords 802 is selected from the search results 801 with a mouse cursor 804 or the like, genes with this keyword 802 (in the figure, “ribosomal”) are marked on the dendrogram with marks 803 or the like” p. 8, line 25 to p. 9, line 3; already cited in claim 6); and displaying the highlighted keywords together with said function group of biopolymers (Fig. 8; already recited in claim 6) thereby confirming biopolymers sharing said one of said functional characteristics are grouped in the selected subtree (“whether the grouping was successful or not is confirmed by focusing on the functions of genes or keywords derived from gene names to see whether relative genes are assembled in a subtree” p. 4, last 2 lines to p. 5; “Keywords contained in the subtrees can be displayed in order to confirm success of clustering as well as to aid focusing of groupings and to aid selection of a clustering method” p. 5, lines 20-23; “By doing so, types of genes assembled in the subtree can readily be known. When the grouping is found failed, another grouping algorithm or (dis)similarity can be selected for another clustering”) p. 9, lines 3-6).

Claim 6 further recites designating at least one keyword from a keyword dictionary file (p.8, last paragraph; Fig. 8); searching in the selected subtree for biopolymers whose attribute information contains the designated keyword; and highlighting in the display window a location of each of the biopolymers in the selected subtree whose attribute information contains the designated keyword; displaying the highlighted keywords together with said function group of biopolymers in the display window thereby confirming relative biopolymers are assembled in the selected subtree (Fig. 8). Claim 12 recites an additional means for designating keywords from the keyword dictionary file (as already recited in claim 6).

The attribute information includes a unique nucleotide sequence identifier and a description of a corresponding nucleotide sequence, said description includes a source organism, a gene name/protein name, or a function (e.g., “U25064 *Rattus norvegicus* ubiquitin/60S ribosomal subunit ...” in Fig. 1; “*The system is provided with gene data 901 for storing gene information and gene expression patterns*” p. 14, last paragraph).

Applicants respectfully contend that Michaels fails to teach or suggest “displaying the selected subtree [clustered based upon corresponding gene expression data] in a separate display window (claim 1)” or “replacing the selected subtree with an icon 701 in the dendrogram thereby displaying the dendrogram with the icon rather than with the selected subtree (claim 3)” according to the invention.

Regarding claim 1, the “wave windows” 1-4 in Fig. 1a was relied upon by the Examiner (p. 3, last paragraph of the outstanding Office Action) to teach the separate window displaying a selected partial tree of the invention. However, the wave 1, wave 2, etc., show “**average** values of expression patterns of all genes” (footnote to Fig. 1a on page 45: “*For each cluster, the average expression pattern for all genes in the cluster is shown as an inset.*”), rather than the gene expression data of individual genes “*as is.*” The same is true for Fig. 2, which illustrates **average** values of expression patterns. As such, Michaels fails to disclose “displaying the selected subtree [clustered based upon corresponding gene expression data] in a separate display window (claim 1).”

Regarding claim 3, the numerals 1, 2, 3, etc. in Fig. 1b allegedly replacing the wave boxes 1-4 in Fig. 1a were relied upon by the Examiner (p. 4, lines 4-6 of the outstanding Office Action) to teach an icon 701 replacing the selected subtree in the dendrogram thereby displaying the dendrogram with the icon rather than with the selected subtree. However, each of the numerals 1, 2, 3 etc. in Fig. 1b represents individual subtrees clustered based on the

normalized mutual information (Fig. 4; "*The neurotransmitter signaling genes map primarily to Euclidean distance cluster waves 2 and 3, and to mutual information clusters 2 and 4. Similarly, peptide signaling genes map mainly to Euclidian distance clusters C (constant) and wave 1, and to mutual information clusters 1 and 6* (p. 50, 3rd paragraph)," which were created independently from the wave boxes 1-4 in Fig. 1a, and *co-exist* with wave boxes 1-4 in Fig. 1a (as shown in Fig. 4), rather than *replacing* the wave boxes 1-4 in Fig. 1a. Even with Fig. 1b, the numerals 1, 2, 3, etc. are merely used to number the six different subtrees which are still fully displayed in Fig. 1b, rather than replacing any of the subtrees each number corresponding to.

In addition, Applicants respectfully contend that Michaels does not use a second clustering method just for a selected subtree of a dendrogram as recited in claim 2 (p. 4, line 3 of the outstanding Office Action). Rather, Michaels clusters respectively by the Euclidean distance and by the normalized mutual information on the retire data/dendrogram (Fig. 4; p. 50, 3rd and last paragraphs). As such, Michaels fails to disclose "designating a second clustering method, which is different from the first clustering method, for further clustering the biopolymers in the selected subtree in the separate display window." This feature of the invention is intended to obtain desired results by carrying out, on a trial-and-error basis, a 2nd/different clustering method on a smaller set of data from classified clustering results (Fig. 6; "*For example, clusters distant from each other (such as clusters 401 and 402, and clusters 401 and 403 in Figure 4) resulting from the first clustering can be selected and excluded to see a subtree of interest in more detail*" p. 8, lines 5-9).

Applicants contend that Michaels fails to teach or disclose each and every feature of the present invention as recited in independent claims 1 and 3. As such, the present invention as now claimed is distinguishable and thereby allowable over the rejections raised in the Office Action. The withdrawal of the outstanding prior art rejections is in order, and is respectfully solicited.

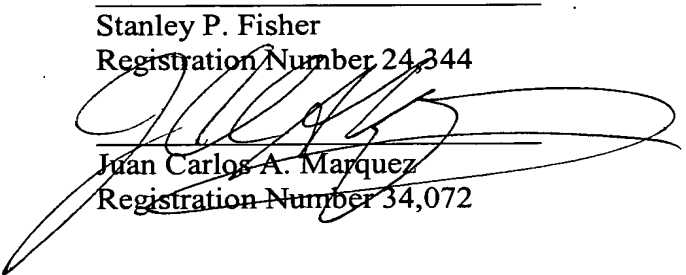
Conclusion

In view of all the above, clear and distinct differences as discussed exist between the present invention as now claimed and the prior art reference upon which the rejections in the Office Action rely, Applicants respectfully contend that the prior art references cannot anticipate the present invention or render the present invention obvious. Rather, the present invention as a whole is distinguishable, and thereby allowable over the prior art.

Favorable reconsideration of this application is respectfully solicited. Should there be any outstanding issues requiring discussion that would further the prosecution and allowance of the above-captioned application, the Examiner is invited to contact the Applicant's undersigned representative at the address and phone number indicated below.

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